

	CGCGATCGTC	GTCAACGAG	TCGACCGTCA	CCACGGACTG	ATCAACAAGT	TCGCGAGCGA	60
	CGCGCGCGCT	GCATCTTCGG	GAGCCCGGAA	CGCGCTCGAC	CGTCCCGAAG	ACGCCCGGCT	120
	GGCTCGCGCTG	CGCGCCATCA	CCGAGCGGCT	GGCCMACGAG	ATGCCCGAGG	TCCAAGCGCG	180
5	CATCGCGGTC	CGCGCAGCGC	AMATCGTCCG	CGCGCAATGC	GGCCCGAAGC	AAAGATTCCA	240
	ATACACCGTC	GTGCGCGAGC	CGTCCAACTA	AGCGCGCCGA	TTGTCCGAAC	TGGCCCAATC	300
	ACACCCCGCG	CGATTGGGTC	TCGCGCGCTC	GGCTCATGGT	CACCCCAATC	AAGGACTACT	360
	TTTGCTCGCG	GCACGACCTC	CGAGAAATGG	CGATTAAGAG	CGCCAAAGCC	CGCGTTGAGG	420
	CGCGCAAGCG	GTTCGCGCGC	CGCGTTCGCG	CGATTCCGAG	TGCTGGCGCTG	ACCGCGGTTG	480
	CGCGCGCGCT	CGGTCAAGCG	CGGTCTCGTC	CGCGATTGAA	GGTTCCGCGC	GTCTGGACCG	540
10	CGACGACCGC	CGCGCGCGAG	CGCGCGGTGC	TGGCGCGCTC	CAAGCGCGCTC	GGAGCGCGCG	600
	CGCGCGCGTA	AGGTTCCGCA	CACCGCGTTG	CGCGGATGCC	GCTCATGGGT	AGCGGTGCCG	660
	GAAGTGGGTC	TAACAAGTTC	GCTGCCCGTC	GATACGGATT	CAAGCGCGACT	GTGATCGCGC	720
	AAACCGCGCG	TGGCGGATGA	CGAACTACTC	TGGTTGATCG	AGGATCGGAT	TGCAAGCATTC	780
	AAAGGGAGGA	ATTCAATAGA	CGTCGCGTTT	TATGACCGAT	CGCAAGCGCA	TGCGGAGCAT	840
15	CGCGCGCGCT	TTTGAAGTGC	AGCGCGAGAC	GGTGGAGGAC	GAGGCTGGCH	GGATGTGGGG	900
	GTTCGCGCGA	AACATTTCCG	GTGCGCGGTC	GACTGGCATC	CGCGAGCGGA	CGTCGTTACA	960
	CACCATGGCC	CAGATGAATC	AGGCGTTTCN	CAACATCGTG	AACCTCTGCG	ACGCGGTTNG	1020
	TGACGGGCTG	GTTCGCGGAC	CGACCAACTA	CGAACACGCA	GAGCAGGCGT	CGCAGCAGAT	1080
	CGTCAGGAGC	TGACCGCGCC	CGACGACTCA	GGAGGACACA	TGACCATCAA	CTATCAATTC	1140
20	GGGACCTTCG	ACGCTCATGG	CGCATGATC	CGCGCTTTGG	CGCGGTTGCT	GGAGCGCGAG	1200
	CATCAGGCGTA	TGATTTTCGTA	TGTGTTGACC	CGGAGTGACT	TTTGGGGGCTG	CGCGGCTTCG	1260
	CGCGCGCTGC	AGGGGTTTCA	TACCGAGTTG	GGCGGTAAGT	TCCAGGTGAT	TTACGAGCGG	1320
	CGCCACCGCC	ACGGGCGAGA	GGTCCAGGCT	CGCGCGAACA	ACATGGCAGC	AACCGGACAG	1380
25	CGCGTGGGNT	CGAGCTGGCG	CTAACCGGGG	TGNTAAATTC	GGTCGGCGCA	CGCGCGCGCG	1440
	ATCAGCTTNG	ACTTTGGCGG	CGGATACAGC	GGCATTTTNT	NGTGGGGAAC	ACTGCGCGCG	1500
	CGTCAGGTCG	CGCGTTTCGCC	TTGTTTGGCG	ACGTGCTCGG	TGATGGCTTT	GACGACCGCT	1560
	TCGCGCGCGC	GGCCAACTAA	TGCGTCCGCG	TTGCTTTGAG	CGCATTCGTC	CGACCGCGCG	1620
	GGCGCGCGGA	GTGTGCTGCT	GAATATAGGA	ATCACGAGAC	GGCGGACAGC	CTCATAGGAG	1680
30	TGAAAGGCTG	CGGTGGCGGG	GGCC				1704

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	CGGCTTTGCG	GTCTGGGCGC	ATTGTGATCT	GGGCCANTTG	CGCCTCCACC	CAGACCGCGC	60
	CGAGCTTGTG	GATCCAGCGC	CGGACCGGGA	TTGCTCAGCG	CGGACCGCGG	AACGAGATTCT	120
45	CGGCTTGATT	CTGGGTGACT	TCGCGATGCG	CGCGGTGATC	CTGTTGGGGA	NCAGCGGTTC	180
	GAACCGGCGT	CNAAGCGGTG	CGGTAAAGCC	AGCGTGTAGC	CGGTCAAGCC	AGCGCGGATG	240
	CGCAATTCCT	TGCGGCGGCA	GCTGAGCGCG	CGCGGCTCCA	CGAAGAGCGT	CAGGTTGAGC	300
	CAGCGACAGC	GATCCAGCGC	GACGATCAGC	CGGAGGTGCC	GAACTTCGGA	CGAGAGGTCG	360
	TGGAAATCCA	GCAATACGCG	CGCGAGCGGA	TCTGTTGGA	CGGAGGAGTC	GGCGAGGAGG	420
50	CGGCAATCCA	GCTTGGCGAT	TTTATCAGAA	ACAGCGAGCG	GGTGGTGGNC	GTGACCGCGG	480
	TGTCCTTCAG	TTTGTGCGAT	GATCAACTGC	ATTCGATGCG	CGAGCTCGCT	TCCGAGCGGTG	540
	AGCGCGCGCT	GTGGCGGCTA	CGCTTCGCGC	TTAGCGGCGG	CGAGCGCGCG	AGCCTTGACG	600
	AGATCGGCGA	GGTCTACGCG	GTGACCGCGG	AACGCAATCG	CGAGTTCGAA	TCCAAGACTA	660
	TGTGGAAGTT	CGCCATTCG	AGCGCTCGAC	AGGCTCTGCG	CGACTATGCT	CGCGAATTTC	720
55	CGACGACCGG	TTTTGAGGTC	CACGCGCAGA	CGGTGAGGTA	CGAGGCTCGC	CGGATGTGGG	780
	CGTCCGCGGA	AAACATTTTC	GGTGGCGGCT	GGAGTGGCAT	GGCGGAGGCG	ACCTCGGCTAG	840
	ACGCAATGCG	CGAGATGAA	CGGCGGTTTC	GCAACTGCTG	GAGCAAGGTC	CGAGAGGTCG	900
	GTACGCGGCT	GGTTCGCGAC	CGCAACAACT	ACGAGCAGCA	AGGAGCGGCT	TCCGACGAGA	960

	TCTCTACGAG	CTGACCCGGC	CCGACGACTC	AGGAGSACAC	ATGACCATCA	ACTATCAATT	1020
	CGGGGACGTC	GACCGCTCAT	GGCCGATGAT	CYCGGCTCTG	GGCGGGTTGC	TGGAGGCGCA	1080
	GCATCAGGCG	ATGATTTCTG	ATGTTTGGAC	CGCGAGTGAC	TTTTGGGGCG	GGCCCGGTTT	1140
5	GGCGGCTCTG	CAGGGGCTTC	TTACCCGAT	GGGCGGTAA	TTCCAGGTGA	TCTACGAGCA	1200
	GGCCCAAGCG	CACGGGACGA	AGGTGCGAGC	TGCGCGACAC	AACATGGGAC	AAACCGGAG	1260
	CGCCCTGCGC	TCCAGTGGG	CTTACCCGG	GTCTTAACT	GGCTCCGCGC	AGGGCGGGCC	1320
	GATCAGGCTG	GACTTTTGCC	CCCGATACAC	GGCGATGTCG	TNCTCGGGAA	CACCTGGCGCC	1380
	GGGTGACGTC	GGCGCTTCCC	CTTGTTCGGC	GACGTGCTCG	GTGATGGCTT	TGACGAGCGC	1440
	TTCGGCGGCT	CGCGCCAGTC	ATTGCTCGGC	CTTGGCTCTA	GGCTCGGCGC	GAATTCGGCA	1500
10	CAGGGGTGCT	GGTGGCGGCT	TATCGGAGC	ACGTGAGCTC	CACGACGAAC	TGATCCAGAT	1560
	GGTGGCTTTC	GGCGAGTTTC	GCATCGGCTC	GTCTGGCGGA	AGGGCGCATC	CCGGCCCATC	1620
	CGGCGCTGAA	GGCGGCTTTC	ATTACACCT	CATCGGCGAC	CGGTCAAAG	AGGGCGGCGC	1680
	GCTCACCGAA	CTGGCCAAAG	TGCGAGATTC	CCAGCTTCTG	GGCTCGGCGA	TGCGGCTGCG	1740
	TGGCGGCTTC	GACCGCCGAG	CATTGTGTTG	GGATGTGTTG	GAGGTGGTTG	AGCTCCGCGC	1800
15	ACGTGCTTGA	CCCAACCGAC	TAGCCAGGCC	AATGAAATTC	GCNCGACCGC	AGAGGTTTTC	1860
	CAGCGAAGTA	CGCGGCTAGT	CGCGCTTGGC	TGCTTCTCTC	GGCTCGGCGC	TCCGGCGGCG	1920
	TCTCTGAGCT	GGCGCTTTC	CGCGACCGCG	GGCTCGGCGA	TGCGCGGCGA	GGCTCGGCGC	1980
	GGGTCTGCTG	GTATGGAAG	CGAGCTGTTG	GGCTCTACGC	AGGCTGGCAT	TGGTCTCACG	2040
	GTGGGTGAGC	TACGGCGCGA	ATCGGCGCTC	CTTGAATGAC	ATTGAGCTTC	CAGGCGCGCG	2100
20	ATTGTTTCCC	AGCTTCGCGA	GGCGGCGGAG	CGAAGCGCTT	TGCGCGGCGC	GACCTTTTTCG	2160
	CTCTGTTGAG	ATTMTCTAGG	CTTCTGAG	CAGCATGGTG	AATATATGAT	CTTCTGCTGAC	2220
	CAGTGAATCGA	GAATCTTTTC	CGCGCTTTAG	ATACGGTCTG	TAGCGCGCGT	TCTGCGGCGT	2280
	GATNTC						2300

23 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	GGGATCTTTC	CCGACCGCG	CCTCGATCAT	CCGCTCTGTC	GGAGCGGTTC	TGCGCGGACA	60
	ACACGACGAA	TGGATGGAAG	GACGGCGCTA	CTTGGGCGTC	GAGGTCTCTA	CCGAGCGCGC	120
	AGCAGCACTG	ACCAGCACCG	AAGAACCGCC	AAGCAGCAAA	CCACTGACAC	CCGAGCACTG	180
40	ACCACTTACG	CTGCCACCGC	AAGGATCAGG	CGAGGAACCT	TCACTCTGTC	ACCACTTACG	240
	TGGCTCTGAG	CTGGTCTCAG	GCCAGCTGCG	AGCCGACCGG	GCTGTGAGTT	TGGCGCTGAT	300
	TGTTGCGCGC	AGCCTGCACC	TTCTGCGCGT	GGGCTTGGC	CTGCTGCTAG	ATCACTTGA	360
	AGTTACCGCC	CACTGCGTGA	ATGAACCGCT	GGCAGCGCGC	CGAAGCGCGC	CCGCGCGCAA	420
	AGTCACTTGC	GGTCAACACA	TACGAGATGA	TGGCTCTGAT	CTCGGCGCTG	AGCAAGCGCGG	480
45	CGTGGCGCGG	GATCATGCGC	CGGTGAGCGT	CGACATCACC	GACTGAGTAG	TTGATGTTCA	540
	TGGAACCTGT	TCTCTTTCGC	TTGTAAAGAT	ATTGTGCTGC	AGCGCTGAGC	GTTAGCTGCT	600
	GAGGATCTTC	TGGAGGGCCT	GCTCTTCCCT	CGTSCCGAAT	TGGGACGAG	AGCGCGCGCT	660
	CGACAAATCT	CTTTAGAGAT	TGCGCAAGGC	CGTTCGACCA	GCATGSGGTT	AGCTGCGCGG	720
	CGCGGCGCGC	TGGCAACCGT	TCCCGCTGGA	GAAAGACCTG	GGGAGATACC	AGTACAAAC	780
50	GACCTCCGAG	ACGTGCTGGA	GCGTGAAGCG	GGTCCACGTC	CGGCTCTCTC	CTTGGCGGCG	840
	CCGCGCTTTC	CAGAGCTGTC	GCTTTACAC	GGGCGGCGCT	ACGACCTGAG	TGATGAGATT	900
	TGCAAGCATC	CGCGCGCGC	CTTTTTCATT	GGGCGGAGCA	AGAAGCGCGA	CATCACGCGA	960
	ATGCTCAAGT	CGTACAGATG	TGATCGGCGG	ATTGTGAGCG	GAATCTGAGC	CGAGAGGTAC	1020
	GGGTGCGGCG	GGGAGCGCAC	CGCTAGGAGC	ATTCACGCGA	AGCGCATATC	ACCGGCTATT	1080
55	CTGTTCAAAG	ACGATCTCAA	CAGCTGCGCG	GACACCGCGA	AGTATCGATG	AGCAAG	1140

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 967 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- | | | |
|----|---|-----|
| 10 | THAGGCCCAA CCTACCGTC GTTTCCTCAC ACCGACCCCA TGGCCTGCTC GCGGAGCTGC | 60 |
| | CGCTAGGGTC GCGGATXACT CCGGCTAGCG CCGCCTTTGC CCACCGATAT GGGTTCCTTC | 120 |
| | ACAGTGTGGT TGCCGCCCGC CCATCGGCGG GATAACGCCA TGACCTCAGC TCGGCAGAAA | 180 |
| | TGACCATGCT CCCAAGGCG TGAGCACCGC AAGACAACCTA AGCAGGAGAT CGCATGCGCT | 240 |
| 15 | TGTGACTAC CCACCCAGAA GCACTGGCGG CCGCGGCCGG CAGTCTGCAG GGAATCGGCT | 300 |
| | CGGCATTGAA CCGCCAGCAT CGCGCTCGCG CCACTCCGAC GACCGGGGTG GTCCGCGCGC | 360 |
| | CGCCGATGAA MTGTCGCGCG TGACGGCGCG TCACTTCGCG GCACACCGCC ABATCTATCA | 420 |
| | GGCCCTCAGC GCGCAGGCGG CCGGCAATCA CAGATGTTTC GTCAACACTC TACAGATGAG | 480 |
| | CTCAGGCTCG TATCTCTCTA CCGAGGCGCG CAACGCGGCG GCGGCTCGGT AGAGGAATCA | 540 |
| 20 | CTGCGATGGA TTTTGGGGCG TTGCGGCCGG AGGTCAATTC GGTGCGGATG TATGCCCTTC | 600 |
| | CTGCGCTCGG ACCAATGCTC GCTGCGCGGT CGGCCCTGAA CCGGTTCGCG CCGGAGCTGA | 660 |
| | GTTCGCGCGC CACCGGTAT GAGACGCTGA TCACTCAGCT CAGCAGTGAAG GGTTCGCTAG | 720 |
| | GTCCGCGCTC ACCCGGATG GCGGAGCGAG TTGCGCCGTA TGTGCGCTGG ATCAGTCCGC | 780 |
| | CTCGCGCGCA AGCGGAGCAG CCGGCCACAC AGCGCAGGCG CCGCGCGGCT GCTTTTGAAG | 840 |
| 25 | CGCGCTTTGC CCGGACGCTG CTTCCGCGCT TATTCGCGCG CACCGCGGCT TCGTTGATTC | 900 |
| | ACCTGATCTC GACGATGCT TTTGGTCAAG ACACCTCGCG GATCGCGGCC GCGGAAGCTC | 960 |
| | AGTACCG | 967 |
- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- | | | |
|----|--|-----|
| 40 | TGGATTCCGA TAGCGGTTTC GCGCCCTCGA CCGGCGACCA CCGCGCGCAG GCCTCCGAAC | 60 |
| | GCGCGCGCGG GACGCTCGGA TTCCGCCGGA CCGCAACCAA AGAACGCGCG GTCCGCGCGG | 120 |
| | TGCGGCTGAC CGCACTGACC GGTGATGAGT TCGGCAACCG CCGCCGATG CCGATGCTTC | 180 |
| | CAGGACCTTG GAGGACAGCG AGCAACGAGC CAGGAGGCGC CGAGGATGCG GCGAGAGGCG | 240 |
| 45 | GAGGCGCGCG CTATCCGCGC GACGCGGAGT AACCGAATTC CGAATCAGCT GAGACCGCTAC | 300 |
| | CGGTGCAAGG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCACAG TTGGTTCGCT | 360 |
| | CCCATGCGCG GTTTCGCGCC AAGCGCGGCG TGATTCGGCA CACGATCGGT CAGGCCGAGC | 420 |
| | AGCGCGCGAT GTCGGCTCAG CGCTTTCAC AGGGGAGATC GTCGCGCGCG TTTCAGGCGG | 480 |
| | CCCATGCGCG GTTTCGCGCG GCGCGCGCGA AATCAACAG CTGTTGAGAT GTCCGCGAGG | 540 |
| 50 | CGAATCTGAG TGAGCGCGCG GATACCTATG TGGCGCGCGA TGCTG | 585 |
- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5 Ala Leu Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Ala
1 5 10 15
Leu Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val
20 25 30
10 Met Ser His Tyr Gln Ala Val Ala His Glu Ile Trp Cys Leu His Gln
35 40 45
Xaa Ala Ser Ser Gly Lys Pro Trp Ala Ser Ile Thr Thr Gly Ala Pro
50 55 60
15 Gly Ser Pro Ala Ser Thr Thr Arg Ser Arg Thr Pro Leu Val Ser Thr
65 70 75 80
Asn Arg Xaa Val Xaa Ala Pro Ile Val Ser Pro Asn His Thr Gly His
85 90 95
Arg Pro Glu Lys Gly Leu Gly Ser Xaa Gln Arg Arg Leu Ser Arg Val
100 105 110
20 Leu Pro Arg Ile Ile Asp Arg Pro Ala Gly Pro Xaa Gly Pro Pro Leu
115 120 125
Thr Ser Gly Ser His Phe Leu Cys Ser Trp His Gly Tyr Ser Ser Gln
130 135 140

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

35 His Ala Leu Ala Ala Gln Tyr Thr Glu Ile Ala Thr Glu Leu Ala Ser
1 5 10 15
Val Leu Ala Ala Val Gln Ala Ser Ser Trp Gln Gly Pro Ser Ala Asp
20 25 30
40 Arg Phe Val Val Ala His Gln Pro Phe Arg Tyr Trp Leu Thr His Ala
35 40 45
Ala Thr Val Ala Thr Ala Ala Ala Ala His Xaa Thr Ala Ala Ala
50 55 60
45 Gly Tyr Thr Ser Ala Leu Gly Gly Met Pro Thr Leu Ala Glu Leu Ala
65 70 75 80
Ala Asn His Ala Met His Gly Ala Leu Val Thr Thr Asn Phe Phe Gly
85 90 95
50 Val Asn Thr Ile Pro Ile Ala Leu Asn Glu Ala Asp Tyr Leu Arg Met
100 105 110
Trp Ile Gln Ala Ala Thr Val Met Ser His Tyr Gln Ala Val Ala His
115 120 125
Glu Ser Val Ala Ala Thr Pro Ser Thr Pro Pro Ala Pro Gln Ile Val
130 135 140
55 Thr Ser Ala Ala Ser Ser Ala Ala Ser Ser Ser Phe Pro Asp Pro Thr
145 150 155 160
Lys Leu Ile Leu Gln Leu Leu Lys Asp Phe Leu Glu Leu Leu Arg Tyr
165 170 175

	Leu	Ala	Val	Glu	Leu	Leu	Pro	Gly	Pro	Leu	Gly	Asp	Leu	Ile	Ala	Gln
				180					185						190	
	Val	Leu	Asp	Trp	Phe	Ile	Ser	Phe	Val	Ser	Gly	Pro	Val	Phe	Thr	Phe
			195					200					205			
5	Leu	Ala	Tyr	Leu	Val	Leu	Asp	Pro	Leu	Ile	Tyr	Phe	Gly	Pro	Phe	Ala
			210					215					220			
	Pro	Leu	Thr	Ser	Pro	Val	Leu	Leu	Pro	Ala	Val	Glu	Leu	Arg	Asp	Arg
						220					225					240
10	Leu	Lys	Thr	Ala	Thr	Gly	Leu	Thr	Leu	Pro	Pro	Thr	Val	Ile	Phe	Asp
					245					250						255
	His	Pro	Thr	Pro	Thr	Ala	Val	Ala	Glu	Tyr	Val	Ala	Gln	Gln	Met	Ser
					260					265						270
	Gly	Ser	Arg	Pro	Thr	Glu	Ser	Gly	Asp	Pro	Thr	Ser	Gln	Val	Val	Glu
					275				280							285
15	Pro	Ala	Arg	Ala	Glu	Phe	Gly	Thr	Ser	Ala	Val	His	Gln	Ile	Pro	Pro
					290			295					300			
	Arg	Pro	Ala	Asp	Thr	Arg	Arg	Ala	Cys	Arg	His	Arg	Asp	Asp	Val	Pro
						310					315					320
	Arg	Asp	Ser	Arg	Ile	Ala	Gln	His	Arg	Asp	Gly	Ala	Gly	Leu	Asp	Pro
					325						330					335
20	Thr	Glu	Arg	Gly	Thr	Ser	Glu	Gly	Asp	Gln	Gly	Leu	Val	Ser	Gly	Trp
					340				345							350

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
1      5      10
Ala Val Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
15     20     25     30
Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
20     35     40     45
Ile Thr Gln Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
25     50     55     60
Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
30     65     70     75     80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala
35     85     90     95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
40    100    105    110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
45    115    120    125
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly
50    130    135    140

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1      5      10      15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
20     25     30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
35     40     45
Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
50     55

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1           5           10           15
Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val
 20           25           30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
 35           40           45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50           55           60
Tyr Glu Gln
 65

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
 1           5           10           15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Gln Ala Arg Arg
 20           25           30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
 35           40           45
Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
 50           55

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1           5           10           15
Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val
 20           25           30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
 35           40           45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50           55           60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65           70           75

```

65		70		75		80							
Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala
		85						90					

5 (2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

15 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn
1 5 10 15

Tyr Glu Gln Gln Gln Ala Ser Gln Ile Leu Ser Ser
20 25 30

(2) INFORMATION FOR SRC IS NO: 21:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (44) MOLECULE TYPE: peptide

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35	Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
	1			5					10						15	
	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Gln	His	Gln	Ala	Ile	Ile
				20					25					30		
	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
			35				40					45				
40	Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile
	50					55						60				
	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Iys	Val	Gln	Ala	Ala	Gly	Asn
	65					70					75					80
45	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala		
					85					90						

(2) INFORMATION FOR SEQ ID NO:23:

50 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STANDARDS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SHO ID NO:22:

Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp
 1 5 10 15
 Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn
 20 25 30
 5 Gln Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly
 35 40 45
 Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln
 50 55 60
 10 Gln Ile Leu Ser Ser
 65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Gln His Gln Ala Ile Ile
 20 25 30
 Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
 35 40 45
 30 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Glu Gln Ala Asn Thr His Gly Glu Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 35 Asn Met Ala Gln Thr Asp Ser Ala Val Xaa Ser Ser Trp Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Met Ala Glu Ala Thr Ser Xaa Asp Thr Met Thr Gln Met Asn Gln
 1 5 10 15
 Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu
 20 25 30
 Val Arg Asp Ala Asn Xaa Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln
 35 40 45
 55 Ile Leu Ser Ser
 50

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1           5           10           15
Ile Arg Ala Gln Ala Gly Ser Leu Gln Ala Glu His Gln Ala Ile Ile
15          20          25          30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35          40          45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Xaa
50          55          60
Tyr Gln Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
20          65          70          75          80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85          90

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Thr Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1           5           10           15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
40          20          25          30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
35          40          45
Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe
50          55          60
Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg
45          65          70          75          80
Asp Ala Asn Asn Tyr Glu Gln Gln Glu Ala Ser Gln Gln Ile Leu
85          90          95
Ser Ser

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

5 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 Ile Arg Ala Xaa Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
 20 25 30
 10 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
 35 40 45
 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Gln Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 15 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30 Arg Phe Glu Val His Ala Gln Thr Val Gln Asp Gln Ala Arg Arg Met
 1 5 10 15
 Trp Ala Ser Ala Glu Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala
 20 25 30
 35 Xaa Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg
 35 40 45
 Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp
 50 55 60
 Ala Asn Asn Tyr Gln Gln Gln Gln Gln Ala Ser Gln Gln Ile Leu Ser
 65 70 75 80
 40 Ser

(2) INFORMATION FOR SEQ ID NO:29:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

55 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
 20 25 30
 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala

35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Gln Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SENSENCE DESCRIPTION: SDO ID NO:39:

20 Gln Glu Gln Ala Ser Gln Gln Ile Leu Ser Ser
 1 5 10

(2) INFORMATION FOR GEO ID NO: 31:

25 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(S) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35	Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
	1			5					10						15	
	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
				20					25						30	
	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
			35					40					45			
40	Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile
		50					55						60			
	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn
		65				70				75						80
45	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala		
					85					90						

(2) INFORMATION FOR GEO ID NO: 32:

50 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala
 1 5 10 15
 Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala
 20 25 30
 Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
 50 55 60
 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
 65 70 75 80
 Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
 85 90 95
 Ala Ala Gly

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala
 1 5 10 15
 Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala
 20 25 30
 Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
 50 55 60
 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
 65 70 75 80
 Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
 85 90 95
 Ala Ala Gly

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Met | Ala | Gly | Arg | Phe | Glu | Val | His | Ala | Gln | Thr | Val | Glu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Glu | Val | His | Ala | Gln | Thr | Val | Glu | Asp | Gln | Ala | Arg | Arg |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Thr | Val | Glu | Asp | Glu | Ala | Arg | Arg | Met | Trp | Ala | Ser | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:38:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Glu | Ala | Arg | Arg | Met | Trp | Ala | Ser | Ala | Gln | Asn | Ile | Ser | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:39:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
- 15 Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
- 30 Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
- 45 Ala Gly Trp Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:43:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15

Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:44:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30

Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:45:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

45

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:46:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1					5				10					15

(1) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln
1				5					10					15

(1) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser
1				5					10					15

(1) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5					10					15	

(1) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

5 Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO:51:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

20 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

35 Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

50 Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

10 Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

25 Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

40 Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

55 Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Gln
 1 5 10 15
 Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gln Val Ile Tyr Gln Gln Ala Asn Ala His Gly Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Tyr Gln Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala

1	5	10	15
---	---	----	----

2. INFORMATION FOR GEO ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Glu Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

30 Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Gly Leu Leu Glu
 1 5 10 15

(2) INFORMATION FOR SRO ID NO: 68:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:68:

45 Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Gly Leu Leu Glu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:69:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala
 1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala
 1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Ser Asp Val
 1 5 10 15

35 (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala Gly Leu Leu Gln Ala Glu His Gln Ala Ile Ile Arg Asp Val
 1 5 10 15

50 (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
- 5 Ala Glu His Gln Ala Ile Ile Ser Asp Val Leu Thr Ala Ser Asp
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:74:
- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
- 20 Ala Glu His Gln Ala Ile Ile Arg Asp Val Leu Thr Ala Ser Asp
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:75:
- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
- 35 Ile Ile Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:76:
- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
- 50 Ile Ile Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:77:
- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Ala Leu Asn
 1             5             10             15
10 Glu Ala Asp Tyr Leu Arg Met Trp Ile
    20             25
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Glu Ala Ala Thr Val Met
 1             5             10             15
25 Ser His Tyr Gln Ala Val Ala His Glu
    20             25
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 967 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
TGAGCGCCCAA CCGTACCGTC GCGTCCGTCAC ACGGACCGCA TGCCCTGCTC CCGCGACTGC      60
CGCTAGGGTC GCGGATCACT CCGCGTAGCG CGCGCTTTGC CCACCGATAT GCGTTCCGTC      120
ACAGTGTGGT TGCCGCTCCG CCATCGCGCC GATAACGCCA TGACCTTCAGC TCGGCAGAGAA      180
TGACATATCT CCGAAGAGCG TGAGCACCAG AGACACACTA AGCAGGAGAGT CGCATTCGCT      240
TTGTGACTAC CCAACCTAGAA GCCTCTGGCG CGCGCGCGCG CATCTTCGAG CGAATTCGCT      300
CGCGATTGAA CCGCCAGAAAT CGGCGTCCGG CGACTCCGAC GACCGGCGTG GTCCGGCGCG      360
CGCCGATGAA NTGTCGCGCC TGACCGCGCG TCACTTCGCG GCACACGCGC AGATCTATCA      420
GGCGGTTCAG GCGCAGGCGG CGGCGATTCA CGAGATGTTT GTCAACACTC TACAGATGAG      480
CTCAGGGTGG TATGCTGCTA CCGAGCGCGC CACCGCGCGC GCGCGCGGNT AGAGAGATCA      540
CTGCGATGCA TTTTGGGGCG TTGCGCGCGG AGGTCAATTG GGTGCGGATG TATGCGGTTT      600
CTGCTCGGCG ACCATAGGTC GCTGCGCGCT CGGCTCGGAA CGGCTTGGCC CGGAGCTGAA      660
GTTCGCGCGG CACCGGTTAT GAGACCGTGA TCACTCAGCT CAGCAGTGAG GGTGGGCTAG      720
GTCCGCGCTC AGCGCGGATG CGCGAGCGAG TTGCGCGGTA TGTGGCGTGG ATGAGTGGCC      780
CTGCGCGGCA AGCCGAGCAG CGCGCCACAC AGGCCAGGCG CGCGCGCGCC GCTTTTGAGG      840
CGCGGTTTGC CCGGACGGTG CTTCCGCGGT TGATCGCGGC CAACCGGGCT TCGTTGATGC      900
AGCTGATCTC GACGAGTGTG TTTGGTCAAG ACACCTCGGC GATCGCGGCC CGCGAAGCTC      960
AGTACGG
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr	Gln	Pro	Gln	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly
1			5					10						15

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu	Ala	Ala	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met
1					5					10					15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala Ala Pro
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Gln Asn Ala Ala Ala Ala Pro Thr Thr Gly Val Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu Val Ser Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

5 Ala Ala His Ala Gln Met Tyr Gln Thr Val Ser Ala Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:96:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

20 Met Tyr Gln Thr Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:97:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

35 Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:98:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

50 Ala Ile His Glu Met Phe Val Asn Thr Leu Val Ala Ser Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:99:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Val Asp Thr Leu Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr
 1 5 10 15

10 (2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
 1 5 10 15

25 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Ala Gly
 1 5 10

40 (2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1784 base pairs

(B) TYPE: nucleic acid

45 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATTCGTTCT	GCACGCTA	AATCCGCGG	ACATCGTCC	CGGCGACAC	GAGGTCAAG	66
GCTGCTATG	GCACGCGG	CTGGGCTGGA	TCTACCTCG	TCTCGACCC	AATGTCACG	120
CGCCTCGGT	GGTCTCAG	GGCTCGTTC	ATTCGGTGA	TGCGGAGCG	CAGGCAATG	180
CGATGCGGA	AGCCAGTTC	CTGGCGGAG	TGGTCACCC	GTGATGCTG	CAGATCTTC	240
ACTTTGCTG	GCACACGAC	AGCCAGCGG	ATTCGCTCG	CTACATCTG	ATGGAATCG	300
TGGCGGGCA	ATCGCTCAA	CGCAGCAAG	GTCAAAACT	GCCGCTCGG	GAGGCAATG	360
CCTACCTCT	GGAGATCTG	CCGCGCTGA	GCTACCTGA	TTCATGCGG	TGCTCTACA	420

	ACGACCTGAA	GCCGGAAC	ATCATCTGA	CGGAGAAC	GCTCAAAGTC	ATCGACCTG	480
	GCACGCTATC	CCGATCAAC	TCGTTGCGT	ACCTCTACG	GACCCACGG	TTCCAGGCG	540
	CCGAGATGCT	CGGACCGGT	CCGACGCTG	CGACCGACAT	CTACACCGTG	GGACGACCG	600
	TCGCGCGCT	CACGCTGGAC	CTGCGCACCC	CGCATGGCG	TTATGTGAT	GGGCTACCG	660
5	AAGACGACCC	GGTCTGAA	ACCTACGACT	CTTACGCGC	GTTCCTGCGC	AGGGCCATG	720
	ACCCGATCC	CGGACACG	TTCAACGAC	CGAAGAGAT	GTCCGCGCA	TTTACGGCG	780
	TGTTACGCGA	GGTGTGCGC	CACACACCG	GGTCCGCGG	CCAGGCTATC	AACGATCTTC	840
	AGTCCGAGT	GGTCGACTT	TGGATGGAC	TGCTGCTGC	GCACACGAC	GTGTATCTGG	900
	ACGCGCAGT	GCACCGGAG	AAGCTGACG	CCAACGAGAT	CGTAGCCCG	CTGTCTGTC	960
10	CGCTGTGCGA	TGCGACGAC	GTCCGCGCTT	CGTCTCTGC	GGCCACGCTG	CTCTCCGACG	1020
	CGGTGCGAC	CTTACGACT	TTGCGCGCG	CGCCGACCG	TGCGCTGAC	CGCGACGCG	1080
	TCGATTTC	AGTCTGCTG	AGCTGCGCT	AATGGAATC	CGCGCGCTG	TGGATCTCG	1140
	CGATGTGCT	AAGCCACCC	GAAGACTCG	CGATCTGCT	GAACCGCTG	GCTGCGCTG	1200
	CGCATGTGCT	TGATACCGG	CGGTGCGCG	GCTGCTCAC	GGCGACTAT	ACTCGGCGC	1260
15	CAACACTTC	ACCGAGGTG	TGGATACCT	TCGCGCGAG	CTGGCGCGCA	AGCTCGCCT	1320
	GGCGCGCGC	CGGAACTAG	CGGCGACAC	CGACGACAC	AAGTCTCTG	AGACCGCTG	1380
	GAACGACAC	GAACGCTGA	TCTCGCGCG	TTTGGAGCT	CGCGAGGCG	GGTGGCGCG	1440
	AGGTGATCG	GTGGCGCGC	TGCGCGCGT	CGACGAGTA	CGCGCGACT	CTCGGCTATT	1500
	CACGCGCGA	CGCTGACCA	CGCGCGTAC	TCGTGCTGC	GGCGGCTGA	CGAGTGAAGT	1560
20	CACGCGGGA	CAGATTCGCG	ACCGCGCGC	AAGATTCGAG	CGCTGCGCG	CGACGAGAC	1620
	ACGCGCTGCT	CAGATTCGCG	CCCTGCTGCT	GGTGGCGCG	CTGAGCTGCG	TGAAGGACAA	1680
	CAGCGCGAG	ACCAACGCA	TCTTGGGTT	CGCTTTCAG	AGTCAAGCG	TGGCGCTGCG	1740
	TGTCGCGCG	TCATGCGCA	GCTTGGCGG	GTAAGTCCG	ACTC		1784

25 (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 766 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: sDNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

	ACAACACACT	CGGTGCGCG	CGGTGCGCG	TGATGCTCG	TGATGACGCT	CGTCCCAAG	60
	TCGCGACAG	GTGCGCGCT	CCCAAGAGT	TCTTGGCGCG	GTGCGCGCG	KACCTGCGCT	120
	ATCCTGCTTG	GTGCGCGCT	CGCAAAAGC	CGCAACTTAA	ACCTGCTTAA	ACCTGCGCG	180
40	AAGTTTCTTA	CATTTACCG	CGCAAGCAG	CGCGCGCGC	GAAGATCTCG	TCTTGAATC	240
	CGAAGGCTT	CGGTGCTG	CCGACTGCT	GACCGCGCG	GATATCTCG	AGGCGCGCT	300
	CGCGCGCGC	GTGCGCGCT	TGCGCGCGC	TGCGCGCGC	GACCGCGCG	CGCGCGCGC	360
	GTGCGCGCG	GTGCGCGCT	GTGCGCGCG	GACCGCGCG	CAGACCGCG	TGTTGCGCG	420
	CGATCTCCAG	CGCGCGCGC	CGGTGCGCT	ACCGATTTG	CGAAGCGCG	CGAAGCGCG	480
45	TCATCAGCG	CGGTGCGCG	AAGGATCGC	CCCAATTTG	GGCAACCGC	AGCGCGCGC	540
	ATTACCGCT	NAACAGCTG	GTGAGCTTC	TTTGAATCG	AKCAACCGAT	AGGAGCGCG	600
	CGCGCGCGC	GTGAGCGCG	ACCGATCGC	NCAGTGTG	CACGATTTG	GTATCGCGC	660
	CGAGTCTG	GACCGCGCG	AGGTTCGCG	ATGCGCGCG	GAGGTGAC	AGCGCGCTG	720
50	ACCTGTTGAT	CAGTTTTC	CAGTCCGCG	TGCGCGCGC	CGCGCT		766

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1231 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

5	CGGCACGAGA	ATGTCGCGTG	TGCGTCGATA	GCCACTTGCG	TGTGGTCGCG	CTGCGACGCG	60
	GTACAGCGAG	TGCGCTGGTC	CAGCGCATCG	GCCCGGCGCA	GGAGCGCGAT	GTTGGCCAGA	120
	CCCGGTGTAC	GAGAACCGGA	CTCAGCAGAG	TGTCGGCGCT	GACGGCGGCT	CAGTTCGCGG	180
	CACACGCCCA	GATCTATCAG	GCCGTCAGCG	CCGAGGCGCG	GCGGATTCAC	GAGATGTTTCG	240
	TCACCACTCT	ACAGATGAGC	TCAGGGTCGT	ATGCTGCTAC	CGAGCGCGCG	AAGCGGCGCG	300
10	CGCGCGCGTA	GCGAGCTCAC	TGCGATGGAT	TGTGGCGGCT	TGCCGCGGGA	GCTCAATTCG	360
	GTGCGGATGT	ATGCGCGTTC	TGCGTGCGCA	CCATGCTCG	CTGCGCGCTC	GCGCTGGGAC	420
	GGGTTCGGCG	CGAGCTGAG	TTCGGCGGCG	ACCGGTATG	AGACGGTGA	CAGTCAGCTG	480
	AGCAATGAGG	GGTGGCTAGG	TCAGCGCTCA	GCGGCGATGG	CGAGGCGAGT	TGGCGGCTAT	540
	GTGCGTGGA	TGAGTGGCGC	TGCGGCGGCA	GCGGAGCAGG	CGCGCACACA	GCGCAGGCGG	600
15	GCGCGGCGCG	CTTTGAGGCG	GCGCTTTCGC	GCGACGGTGC	CTCGCGGCTT	GATCGCGGCG	660
	AACCGGCGCT	CGTTGATGCA	GCTGATCTCG	ACGATGTCTT	TGTGTCGAG	CAGCTCGGCG	720
	ATCGCGCGCG	CGAGAGCTCA	GTACGCGGAG	ATGTCGCGCG	AAGCTTCGCG	GCGGATGAT	780
	CGCTAGCGCG	CGAGTTGCGC	GAGCGGCTCG	GCGCTCAGCG	CGTTTACGAC	GCGCGCGGCG	840
	ATTCGCGGCG	CGACCGCTCA	GGGTACGCG	GCGCGGCGCG	TGGCGCGGCG	GCGCGGTACG	900
20	GCGGATGCA	CGCTAGCGGA	GATGATCTCC	GCGCTACCGA	ACGCGCTGCA	AAGCTTCAGT	960
	TGACGCTCT	TGCGATGCT	TACCGTTCG	CTGCTGTCG	TGTGCGAGAT	CTGTTTCGCG	1020
	AGCGCGAGT	TGCGGAGCT	AATTTGCGCA	CTGCTGAGCG	ACCTTCGAGCG	CAGCGCGGCG	1080
	TGTTTATATA	ACGCGCGGCG	CGTGGCGTAC	TTCAGCATCG	GATGCGGCGA	CAGCTTCAGT	1140
	CGCTCGCGCA	AGACCGTGGG	ATGTCGCGCG	TAGCGCGGCA	GCGCTCGGCT	CGCGGNTGCT	1200
25	GCGGATGCGG	CGAAGGCGCT	GCGCTGTCGC	G			1231

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

40	CGGCACGAGC	TGTCGCGGAT	CAGTGGCATT	GAGGCGTTGT	ACGACCTTCT	GCGGATTTGA	60
	ATACCGCAAC	AGGCGGCTAT	CGTTTACTCC	TCAGTAGAGT	ACTTCGAGAA	AGCGCTGGAG	120
	GAGCTGGGCG	CAGCGTTTCC	GGGTGATGCG	TGGTTAGGTT	CGCGCGCGGA	CAGATAGGCG	180
	GGCGAAGAGC	CGAAGCAGCT	GAATTTTTC	CAGGAGCTGA	CGAGCTCGA	TGCTCAGCTC	240
	ATCAGCGTGA	TGCGAGACCA	GCGCAAGGCG	GTCCAGACGA	CGCGCGACAT	CGTGGAGGCG	300
	GCCACGAAAG	GTCTCGAGTT	GTGCGCGCG	GTGCTGTGG	ACCTTACCTA	CATCGCGGCT	360
45	GTGCGGCGCG	CGCTTTCGCG	GCGCTTCGAG	GCGCGTTTTC	GCGCGGCGCG	GATGCGGCTA	420
	GTGCGGCGCG	CGCTTTCGCT	CTTGGTCGTA	AAGAGCTGTA	TCAGCGCGAC	TCAGCTCCTC	480
	AAATTCGCTG	CGAATATTGC	GGAGTTGGTC	GCGCGCGGCA	TTGCGGACAT	CATTTGCGAT	540
	GTGCGGCGCA	TCATCAGGCG	CGTCCCGGGA	GAGGTGTGGG	AGTTCATGAC	AAGCGCGCTC	600
	AACGCGCTGA	AGAGCTTTTG	GCGACAGGTC	ACCGGCTGGG	TGACCGAGCT	GTTCTCTGCA	660
50	GGGTGCTGCA	ACCTCGAGTC	CTCTTTGCG	GCGCTCGCGC	GCTTGAAGCG	GCGGAGGAGC	720
	CGCTTGTGCG	AGGTACTGCG	CTTGTTCGCT	GCGCGCGGTC	GCTGCGGCTC	GTGCGGCTTG	780
	CGTCAAGCGG	ATAGCTTCGCG	GAGCTCAGCC	AGCTTTCGCG	CGCTTGGCGCG	CATTGGGCGG	840
	GGGTTCGCGTT	TTCGCGGCTT	GCGGAGCGCT	CGTCAAGCTC	ATGCGGCTTC	AAGCTCGGCG	900
	GCGCTACGCG	CGCGAGCTGA	TGCGCGCGCG	GCGCGCGCTG	CGGAGCAGCT	CAGCGCGGCG	960
55	TGCGAGCTGG	TCTCGCGGCA	GCGTTCCCAA	GCGTTTGGCG	GAGCGGCTAG	CATGCGGCGCG	1020
	ATGCAACCGCT	CTTCGCGGCG	GTGCAAGAGG	ACGACGAGCA	AGAGGATGCT	GAGAGGCGCG	1080
	GCGCGGCGCA	CTGAGAGAGC	CGAGCGCGCG	CGAGTCGAG	CTGAGCGAGC	CGGTGGCGGA	1140
	AAGTGCTGCG	TACGAGACCT	CGTCTAAGCG	CATGCGGAGC	CAGATCCATT	GTTAGCGGAG	1200

	GCCTACACAC	CGCCAACTCT	AAACCGAAGG	GACACGATCA	ATGACGGAAA	ACTTGACTGT	1269
	CCAGCCCGAG	CGTCTCGGTA	TACTGGCGTC	GCACCATGAC	AACGCCGCGG	TCGATGCTTC	1320
	CTCGGGCGTC	GAAGCTGCCG	CTGGCCTAGG	CGAATCTGTG	GGGATCAGTC	ACCGTCCGTA	1389
5	CTGCTCACAG	TTCAACGACA	CGTTAAATGT	GTACTTGACT	GCCACAAATG	CCCTGGGCTC	1443
	TGCTTTGCTT	ACGGCCGGTG	TCGATCTGCG	CRAAAGTCTT	CGAATTCGGG	CGAAATATTA	1500
	TAGCGAGGCT	GACGAGCGT	GGCGCAAGGC	TATCGACGGG	TGTATTACCT	GACCAAGTTT	1550
	GCTGCCCGCA	GTCCAGGCCA	CGACGTAGCG	CAGGTGCTGT	CCCTCGTACG	CGTGGATCGG	1620
	ACCGGCCAGC	ACGAGCGACC	GGTCCGCAAC	GATGGGCACG	GACAGTAGCT	CGCCCGCATG	1680
10	CCCGGCTCGG	GTTGGCGGCA	CAAAACCGGG	CAGTTCGGCC	TGCGGCAGCA	CGGTGGTGGT	1740
	GGAGCCCAAC	CGGCGACAGG	CGGTAAACCA	TCCCGACCCG	AGCACGACCG	AGACGTGATG	1800
	TTCCCGGATC	CGGTTGGGCT	CAGCGATGAC	CTGGCGCCCG	CGCCGGAGCA	GTTTGTGGGG	1860
	ATCGGCGGCG	GGGTACACCA	CAGTGGGCGA	GCCTTAACGA	CGCCCTCGCC	GGGGAGCGGG	1920
	TGCTGTGCTA	TGAGTACTGT	CGAGCATGCC	AGCAGCCAGC	GCATCGGAGC	CGCTCGAGGA	1980
15	ATTGGTTCGG	CGCCGTGGTG	CGGAGCTGGT	CGAGCTGTCC	CATGCCATCC	ACCTGCTGCC	2040
	G						2043

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

	GAGCTCACCG	CTATCAACCA	ATACTTCTTG	CAGTCCAAGA	TGCAGGACAA	CTGGGGTTTT	60
30	ACCGAGCTGG	CGGCGCACAC	CGGCGGGGAG	TGTTTGAGAG	AAATGCGCCA	CGCGGAGGAA	120
	ATCACCGATC	GCATCTTGTT	GCTGGATGAT	TTGCCGAACT	ACGAGCGCAT	CGGTTCTGTT	180
	CGTATCGGCC	AGACGCTCCG	CGAGCAATTT	GAGGCCGATC	TGGCGATGAA	ATACGAGCTG	240
	TTGAATCTTC	TCAAGCCAGG	AATCGTCTTG	TGCCGGGAGA	AACAGGACAC	CACCGAGGCC	300
	GTACTGTCTG	AGAAAACTGT	TGCCGACGAG	GAGGAACACA	TGCACTACTT	GGAAACGCGG	360
35	CTGGAGCTGA	TGGACAGCT	AGGAGAGGAG	CTTTACTCGG	CGCAGTGGGT	CTCTGGGCCA	420
	CGGAGCTGAT	GCCCGCTTGA	GGATTCTCCG	ATACCACTCC	GGCGCGCGCT	GACCAAGCTCT	480
	AGCATGAGAT	CGAAGACGGA	TGGAGGGGCG	GAATATGGCG	GCOCACAGC	ACCGAGCACT	540
	GCOCACACCG	CAATCGAGGC	CGGTGGGCGG	CTGCTCACTC	CGGTGCGAGC	CAACATATTT	600
	TTCAACGCGA	TTGTGTTGCG	GGTGCCTGTC	CGTGCAGCCG	GCCAAACCAT	CGTTGTGCCC	660
40	GCATTCGCGA	CGATGCTCGG	CGAGCTGGGC	AGCACCGTTG	ACCAATCTGT	GGCGGCTCAC	720
	AGCATCTGCG	TGGGCGAAC	ACTGKYGGKK	GTGKKKSKSK	KSRMRKCTC	GCTGCTCTCG	780
	TGGGCGCAA	CAGGTTGCTG	CTAGGCTCCG	TGCTGGTCTT	GGTCTTTGCG	TGTTGTCTGT	840
	GCGGTTTATC	GCAGACGATG	ACCATGCTGG	CGATCTCTCG	GGCACTGAGC	GGGCTGCGTG	900
	CGGTTGCTAT	TTCCGTCAAC	ACCTAAGGCG	TGGCGCTGAG	GGTGGTCCCA	CTGCGGGACC	960
45	CTGCCCGCTA	CCAGGCGCTC	TTANGTCCGG	TGTTGCTGTT	CAACACGCTC	ACCGGTCGCG	1020
	TGCTGGGCGG	CTGGCTCACG	GACTACTGGA	GCTGGCGGTT	GGCGTTCCGA	CCACACGCCC	1080
	CATCACCGAC	CGGATGCGGG	TCTTCCGCGC	GAACACCGCC	CTGCGCGCGT	TGCGAGGAGG	1140
	TGCTTGGGCG	AACGTGTTCC	CACAGCGCCA	GAACGCTCGG	AAATGCGGAT	GCCGACCCAC	1200
50	AC						1202

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

5  GGGGGGCGCA GTTGGCCAGC AGTTNNGGCG GGGGAGCCCG TTCGUNGACC AAGAAATCCG      50
   CTTGGGCGAAG CAGCCGCGAC GCGGACGCTT GATCGCCGGG ACCGGGCGCG      120
   ACCAAGGCGCA TTCCGCCGNT GAGGAAGTCG GAATNTGTGG CATTGATGAC GCCCTGCTGC      180
   AACGCTGCGC GGATTGCGGA GCGGATCGCC GCGGAACGGC GGTGCTCACC ACCGGGCGAGC      240
   ACCTCTACGC ACAGGCCGCG ATAGCTGAAT GACGCCGGGT NAGCGCGCTC CATTCCACCG      300
10  NGAATTCGGC CCGGAGCGAA AAGATTCGTC GCGCTCGGCT CTGGGCGACG ACAGCCACGT      360
   TCACCCGCGC GTTATCGGTG GCGCCGATCG CATACCAAGC GCCCTCAAGG TGGCCGTGTG      420
   GGTAGTCACG CACCGACCAAG GTGATTTGAT CCATCGCTTN GACCGCGGGG GTGACGCTTG      480
   GGGCGATCAN GTGACAC

```

15 (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

25  TGGATTCCGA TAGCGGTTTC GCGCCCTCGA CCGCGACCA CCGCGCGCAG GCCTCCGAAC      60
   GCGGGGCGCG GACGCTGGGA TTCCCGGGGA CCGCAACGAA AGAACGCGCG GTCCGGGGGG      120
   TCGGGCTGAC CCACTGCGC GGTGATGAT TCAGCAACCG CCGCGCGATG CCGATGGTGC      180
   GCGGACCTGG GGAGCAGGCG AGCAACGAGC CCGAGCGCGC CCAAGGATCG GGGAGAGGGG      240
   GAGCGCGACG CTTACCGCAC GACAGCAGAT AACCGAATTC CGAATCAGCT GACCCCGTAC      300
   GGGTCGAAAG GAGAGATGTT ATGAGGCTTT TGGATGCTCA TATCCCAAG TTGTGCGGCT      360
   CCCAATCGGC GTTTCGCGCC AAGCGCGGCG TGATGCGGCA CAGCATCGGT CAGGCGCGAGC      420
   AGCGCGCGAT GTGCGCTCAG GCGFTTCACC AGGGGAGGTC GTGCGCGCGC TTTCAGGCGC      480
   CCCATGCGCG GTTTGTGGCG GCGCGCGGCA AATCAACAC CTTGTTGGAT GTGCGCGCAG      540
   CGAATCTGGG TGGGCGCGCC GGTACCTATG TGGCGCGCGA TGCTGCGGCG GCGTGCAGCT      600
   ATACCGGGTT CTGATCGAAG CCGTCTGACC GAGAGGACCT GTGATGTGCG AATCATGTA      660
   CAATCTCCCG GCGATGTGG GTGCGCGCGG GGTATGCGCC GGAATGCGCG GCACGCTGCA      720
   GAGCTTGCGT GCGGAGATG CCGTGGAGCA GGTGCGGTTG CAGAGTGCTT GCGAGGCGCA      780
40  TACCGGATC ACOTATCAGG CGTGGCAGGC ACATGCTAA CCAGCGCAGG GAAGATTGG      840
   TCGCGGCTT

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

55  Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
    1           5           10           15
   Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
    20           25           30

```

Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEC ID NO:110:

15 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
25 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

30 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
40 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 222:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (11) MOLECULE TYPE: peptide

(X4) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met
\$5	1				5					10					14

(2) INFORMATION FOR SEC ID NO: 113:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
- 10 Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:114:
- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
- 25 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:115:
- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
- 40 Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:116:
- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
- 55 Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Met | Ser | Ala | Gln | Ala | Phe | His | Gln | Gly | Glu | Ser | Ser | Ala | Ala |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:118:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | His | Gln | Gly | Glu | Ser | Ser | Ala | Ala | Phe | Gln | Ala | Ala | His |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:119:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Ser | Ala | Ala | Phe | Gln | Ala | Ala | His | Ala | Arg | Phe | Val | Ala |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |
- (2) INFORMATION FOR SEQ ID NO:120:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Gln | Ala | Ala | His | Ala | Arg | Phe | Val | Ala | Ala | Ala | Ala | Lys | Val |
| 1 | | | | | 5 | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
 1 5 10 15
 Asp Ala

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1752 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGCACGAGA ATGTCGCGTG TGCTCGATA GCCACTGCG TGTCGTGCG CTGCCAGCGG 60
 CTCAGCGCAGG TCGCTGCTGC CAGGCCATCG GCCCGCGCA GAGCGCGCAT GTTCGCGAGA 120
 CCGCGGTGTC GAGAACCGGA CTCGACGAA GTCGCGCGCT GACGCGCGCT CAGTTCGCGG 180
 CACACGCGCA GATCTATCAG GCGCTCACCG CCGAGCGCG GCGGATTCAC GAGATGTTGG 240
 TCAACACTCT ACAGATNANC TCAGGCTGCT ATGCTGCTAC CGAGGCGCGC AAGCGCGCGG 300
 CGCGCGCGTA GAGGATTCAC TCGGATGGAT TTTGGGCGT TCGCGCGCGA GGTCAATTCG 360
 GTGCGGATGT ATGCGGCTCC TGCTCGGCA CCAATGTCG CTGCGCGCTC GCGCTGGAAC 420
 GGGTTCGCG CGGAGCTGAG TCGCGCGCGC ACGGTTATG AGACGCTGAT CACTCAGCTC 480
 AGCAGTGAAG GTTGCTGAG TCGCGCGTCA CGCGCGATGG CCGAGCGAGT TCGCGCGTAT 540
 GTGCGCTGGA TGAGTGGCGG TCGCGCGCAA GCGGAGCAGG CGGCGCACGA GCGCGAGGTC 600
 GCGCGCGGCG CTTTGGAGCG GCGGCTTGCC GCGAGCGTGC CTCGCGCGTT GATCGCGGCG 660
 AACCGCGTTC CTTGATGCA GCTGATCTCG ACGAATGTCT TTGATCAGAA CACCTCGGCG 720
 ATCGCGCGCG CGGAGCTCA GTACGCGCGG ATGTGGCGCC AAGCTCTCGC GCGGATGAT 780
 GCGTACGCGG GCGGTTGCG GAGCGCTCG CCGGTCACCG CGTTTACGAC GCGCGCGCAG 840
 ATTCGCAACC CGACGCTCA GCGTACGCG GCGCGCGCGG TGGCCACCGC CGCGGATACC 900
 GCGCGATGCA CCGTACGCG GATGATCTCT GCGCTACCCA ACGCGTGCA AAGCTCTACC 960
 TCACGCTGCT TCGGATGCT TACGCTGCG CTGCTGCGG TGTGCGAGAT CTGTGTCGCG 1020
 ACGCGCAAT TCGCCGCTTC AATTTCGCG CTGCTGACG ACGTGCAGCC CTACGCGAGC 1080
 TTTTNTATA ACACCGAGG CCGCGCTAC TCGACGATG GCATGCGCAA CAACTCTGTT 1140
 CAGTTCGCGA AGACCTCGGG ATTGATCGGC TAGCGCGCAC CGGCTCGGCT CCGCGCTGCT 1200
 CGGATGCGCG CGAAGGCGTT GCTTGGACTG GCGCGGATGC TCGGTGCGCG CGCGGTGCGG 1260
 GCGGATCTGG CCAATGCGGG TCGGCTGCG AAGCTGTCG TCGCGCGCGT GTTGANTGGA 1320
 CGGTTGCGCG GCTCGGTCAC TCGCGGCGCT GCTCGGCTAC CGGTGAGTAC GGTCAATGCG 1380
 GCGCGCGAGG CGGCGCGCGG AAGCTGTTT GCGCGCGCTC CGCTATCTGG TCGCGCGCGG 1440
 GCGCGCGCGG GTCCACGCTA CGGATTCGCT CCGACGCTA TGGCTGCGCC ACCCTTGCGC 1500
 GCGATGTCG CTGCGCGAAC GTATTACGC GCGCGCGCTG GCTGATGTTG TCGGTGCGGG 1560
 GTGCAATTC GTGCGCGCGG AATCTCTGCT GGGTTATTTC CGGTGCGGAT TTTTCGCGAA 1620
 GCGCGGTTCA GACCGCGATT TCGTAACGGT CCGCGCACTC TCGTTCGCGA TCGCGCACTA 1680
 AGTGACGCTC GCGCGAACC CGTTGCGTNT GAAAGCTTCA GAAAGCGCGG CTGCCACGCG 1740
 TTCGCAACAC GG 1752

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

	Met	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Val	Asn	Ser	Val	Arg	Met	Tyr
	1				5					10					15	
5	Ala	Gly	Pro	Gly	Ser	Ala	Pro	Met	Val	Ala	Ala	Ser	Ala	Trp	Asn	
			20						25				30			
	Gly	Leu	Ala	Ala	Glu	Leu	Ser	Ser	Ala	Ala	Thr	Gly	Tyr	Glu	Thr	Val
		35					40					45				
	Ile	Thr	Gln	Leu	Ser	Ser	Glu	Gly	Trp	Leu	Gly	Pro	Ala	Ser	Ala	Ala
	50					55					60					
10	Met	Ala	Glu	Ala	Val	Ala	Pro	Tyr	Val	Ala	Trp	Met	Ser	Ala	Ala	Ala
	55					75				75					80	
	Ala	Gln	Ala	Glu	Glu	Ala	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Ala	Ala
				85					90						95	
15	Phe	Glu	Ala	Ala	Phe	Ala	Ala	Thr	Val	Pro	Pro	Pro	Leu	Ile	Ala	Ala
	100								105							
	Asn	Arg	Ala	Ser	Leu	Met	Gln	Leu	Ile	Ser	Thr	Asn	Val	Phe	Gly	Gln
		115						120					125			
	Asn	Thr	Ser	Ala	Ile	Ala	Ala	Ala	Glu	Ala	Gln	Tyr	Gly	Glu	Met	Trp
	130				135							140				
20	Ala	Gln	Asp	Ser	Ala	Ala	Met	Tyr	Ala	Tyr	Ala	Gly	Ser	Ser	Ala	Ser
	145				150					155					160	
	Ala	Ser	Ala	Val	Thr	Pro	Phe	Ser	Thr	Pro	Pro	Gln	Ile	Ala	Asn	Pro
				165					170						175	
25	Thr	Ala	Gln	Gly	Thr	Gln	Ala	Ala	Ala	Val	Ala	Thr	Ala	Ala	Gly	Thr
		180						185					190			
	Ala	Gln	Ser	Thr	Leu	Thr	Glu	Met	Ile	Thr	Gly	Leu	Pro	Asn	Ala	Leu
		195					200						205			
	Gln	Ser	Leu	Thr	Ser	Xaa	Leu	Leu	Gln	Ser	Ser	Asn	Gly	Pro	Leu	Ser
	210					215						220				
30	Trp	Leu	Trp	Gln	Ile	Leu	Phe	Gly	Thr	Pro	Asn	Phe	Pro	Thr	Ser	Ile
	225				230					235					240	
	Ser	Ala	Leu	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Ala	Ser	Xaa	Xaa	Tyr	Asn
				245					250						255	
35	Thr	Glu	Gly	Leu	Pro	Tyr	Phe	Ser	Ile	Gly	Met	Gly	Asn	Asn	Phe	Ile
		260							265						270	
	Gln	Ser	Ala	Lys	Thr	Leu	Gly	Leu	Ile	Gly	Ser	Ala	Ala	Pro	Ala	Ala
		275					280						285			
	Val	Ala	Ala	Ala	Gly	Asp	Ala	Ala	Lys	Gly	Leu	Pro	Gly	Leu	Gly	Gly
	290				295							300				
40	Met	Leu	Gly	Gly	Gly	Pro	Val	Ala	Ala	Gly	Leu	Gly	Asn	Ala	Ala	Ser
	305				310					315					320	
	Val	Gly	Lys	Leu	Ser	Val	Pro	Pro	Val	Trp	Xaa	Gly	Pro	Leu	Pro	Gly
				325					330						335	
45	Ser	Val	Thr	Pro	Gly	Ala	Ala	Pro	Leu	Pro	Val	Ser	Thr	Val	Ser	Ala
		340						345						350		
	Ala	Pro	Glu	Ala	Ala	Pro	Gly	Ser	Leu	Leu	Gly	Gly	Leu	Pro	Leu	Xaa
		355					360						365			
	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Gly	Pro	Arg	Tyr	Gly	Phe	Xaa	Pro	Thr
	370				375					380						
50	Val	Met	Ala	Arg	Pro	Pro	Phe	Xaa	Gly	Ile	Val	Ala	Ala	Ala	Thr	Tyr
	385				390					395					400	

(2) INFORMATION FOR SEQ ID NO:127:

- 55 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGCACGAGCA CCGATTGACC GCGGAAAGAC CTGACCGCCC CACCCAGCGC GCGCCGCGATC 60
 ACCGCGCCCG TCCGACGAAC CTTTTGGGTA AACGAGCCAC TCCAGCGGAG ATCGGTACCG 120
 CCCAGCGCAT TTGCTGTAAAG GACCACTCTG CCGAAGTAGT CCTGGACGGG TGTCTCTGCG 180
 10 CCAACAGCAT GTAGAGGCTG GCGAGCGTTC TGCTCATACT CGAGCGTTCT TCTCTGCAAG 240
 AACACCGGCG ACATGCGCTAG TTTCGCGATG GCGCCGATGC CCGCGCGCGC GCGATCACCG 300
 TCTCGCGCCC AACTGATTTA AGCAACGATG CGCTTGGCCC AGGTGCGCCA GTTGCACCG 360
 TCTGTACGGA GCGGAACAA GGTTCGAGCC GCGCGCGCTG TGTCTTGT GACCTCGAAC 420
 GAAATTTTCC GACCGGACAT GCGCGACTCC GGAACGACA ACTGAAGCTC GTGC 474

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCGCGCGG GAAAGAAATA TTACTGGCAG GACCGGCAGA ATGCATGGTG ATATTCGGGT 60
 GAGGAGGCGG CCGAGGAACC GACTAGTGCG AGGGTCACAC CATCGTTAT TCGTTGCGGT 120
 30 TTGCGTCTTG GATCTGCGGG UCCGCGCAGG AGTTGGCAGG ACCGCTGACG CGAGCGCTGT 180
 TGACAGAGTC GGTTCAGCTC GAATCTGCCA CCGCTCAGAT CGGAGATGTA GGCACATCG 240
 CCAACACATC GACCGCGTTC AAGTCCGCGT CCGTGGCTAC GACCGCGACC CTTTCGACG 300
 TGCGAACCGG AGCGCGCTTC ACCGACCGGG ACCGAGATCG TCGGTGGTGT CCGCGATGAG 360
 CGTTGCGAGG TGCGCGGTTC AATCCCGCAT CTGCTTGCGT ATGCGGAGAC CGCGCGAGCG 420
 35 GCTGCTGTCG ACTCAACCAT CGCGCGCGTG CGGCTGCGCT GCGGTCAGCA GCGCAACCGG 480
 TTTCGCGCTG GCAGTGTATG TGATGTCTTC GCGCGCGTGC ACGCGCGGTA SCAGCGCGCT 540
 GGTGTTGTTG CGCAGTTGCG GAGACGCGAC TTGACGAGCG AGCTCGCGGG GATCGGCTTG 600
 CGCTGGGCGC GGTGTACCG TCAATCGCTT GGAATATCAC GTGATCTATC GCGCGAGAGC 660
 CGCGGATGTA GCGAGGCAAA CGGCTTACAC GCGCTGCTTC GCGTTGACCG CCGCGAAGCT 720
 40 TACTGTGCGG GGGGATCGAG CACCGATCGC ATCATGTACA CCGTCCGCTG GCGGCTGTGA 780
 CTGCGCACCA TACCAACGCG CGCTTGTGA CCGTGGTTCG TCGCGCGCGC CTATCACCGT 840
 CAGCTCGGCA CCTTCAGGCT CTGATCGGTC CCGTGGATCC TCGTCGAGCT CCGCTGCGCG 900
 GCTATCAGCT GGTAGGTCAG GATGCTGCTG AGCACTCTGG CGTCACTCTT GAGTTGATCG 960
 ATAGTATGCG CCGGACGCTT GTGGAATGCG CGCTTGTGCG GCGCGAAGAC CGTGTACTCG 1020
 45 CCGCGCTTGA GGTGTTCGAG CAGATTACCA TCGGCTTCA GCTTGCCTGA CAGAGCCGAG 1080
 GTCAAGGTCG TGAGCATCGG GTTGTGGAAG CGCGCGGTAG CGACCGGGTC TTGCGCGATT 1140
 CGCGGCAACG ATCGCGGACC GGTGGGATTT TGCGCGCGGT ATTGCGGCGA CCGACGACCA 1200
 ATCAGGCTCG TCGCGCTCAG CCAATGCGGC CGTGTGTAAG GCGGCTCGCG GCTTGTGCG 1260
 CGCTTTCGCG CTGCTGCTCT CCGACACCGG TTGCTGCTCT GAACACCGCG CTAGAGACCG 1320
 50 AATGCGGAGG GCTGCGAGCG TGCTGCTGCG GCGCGGTTG GCGTGAACCT TGATCATCG 1380
 TCGATCTCT TTGCTCTTSC GCGCGGCTTG AACCGCGTCC TCTTGGGTGG A 1431

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGAGAGT	CGTATCTTTC	CACCCAGGCG	CGGTAGGAAA	CGCTGGCCCT	GGTTAACTCA	60
GATGCGGGCG	GCCGTCGATT	CGAGAGGTAA	CCGATCGCCC	GGCGACAATG	GTTTACCCAC	120
CGAGACTGAT	TGCCCGCCAG	CGCGCTTCGA	CGTGAAGCCG	CCGCTTCGCG	CATGCGCCGA	180
ACCGCTCGAC	TCAACGACCT	TCTACATAGT	ACGTACCGCA	CTTTACCGCA	TTATCGCTGA	240
CGATCTTTGC	CTCCACGGAC	TCCAGAACTC	ACTCGTGGC			279

(2) INFORMATION FOR SEQ ID NO:130:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACCGCCACCC	CGAGCCCGGA	ATCACCGTCG	GTAACTGCG	AATACATTT	CTTCATCGAC	60
GACTTGGAGC	ACAGCGCAAC	CGAGCCCAAC	GCTTCATAGC	CTTCTTCCTC	GATCTTCCAA	120
CCGCCCGGCG	CGTCAACGGA	AACGATACGA	CCCTGCTCTT	CGCGGTGAGA	CGCATGAATG	180
TCGTATCCCG	CGAGCAACCG	CAACGCCAGC	AGGCCCTGCA	TCCGCGCCGC	CGATTTGCCA	240
CGACGCATAA	TCCCGACGCG	GTTGATTTTC	CCGCGCAACG	TGACGCGCAC	ACCTTCGAGC	300
TTCTCGTAGT	GCTCAAGTTC	CACCGCATAC	AGCCCGGCAC	ACTCAACCCG	GACCCGACCC	360
GTCCACGCGA	TGCCCGTAGC	GGTGTAGTCA	TCCGTATAT	ACACCTTCGG	CACATTCACG	420
CTCAAAATCA	TGTTGCCCTG	CGTTCGACGC	CGGTCAACCG	CCATGACACG	ACCGCCCGCG	480
TATTTACGCG	CGACAATGAT	GTTCCCGTTC	GGCAGTTGCG	CATCGCCGCC	TCCGAGTGGC	540
GCACCGCCCG	TGATGCTTTC	CGCGACGAC	TCCGCGGCTT	GGCGGCGGAG	GAGTCAAGT	600
GAAGAGAGAT	AGGTTCTACG	CGGCTGTTC	AGAGAGTGAA	TGATGAGACA	GGCGATCGGG	660
CAACGCGCG	GTCATCTTCC	GCTCTTTTTC	AGTATCTGCG	GGACGAGTTC	CTCCGCGTTC	720
TCTCTGAGGA	CGTCTCGAT	TTCCTGAGAC	AGATCTGCG	TCTCTCGGCT	CACTCTTTTC	780
CGACGCTGCT	TCCGCGCGCG	GGTCTGCGCG	CGATCTGCT	CATCATCGCC	GGCGCCACCG	840
CGACGCTGCG	TGCTCTCTTC	CGGATGCGCC	GCTCTGCTCT	TCTCATGCGC	CTTTCAAAAG	900
CGCGCGCGGT	CGCGTCAAC	CGCCGCTGTC	TTTCTCTCAC	CTACCGGTCA	AGACCAACGT	960
TTCCCGCGCT	AACGAGGCTT	AGCGAGGCTC	AGCGGTGAGT	TGCTCTACCA	GCTTCAACGC	1020
ACTGTCCACG	GAATCCAGCA	ACGCAACGAC	ATCGGCTCTA	TACCCCGGCA	ACGCTCCGAG	1080
CGTCCGAGAT	CGACGACGCG	AGTCCGCGCC	AGTTCGAGGA	TGACCGAGTC	CGAGCTAGCC	1140
CGCGCGATAT	CAGCCCCGAA	CGGCGCGAGG	CATTTTCGCG	CGGAAATACG	CGCGGGTGTG	1200
GCTCGAGCGT	TCTCCACGCG	ACTCAGCACG	TGTTTCTTCG	GTGACTAAGC	GCTTTATCGA	1260
CGCGCGCGCG	ACCAACCGGT	TGTACAGGCC	CTTCTGCGAG	CGGACATCGG	AGTACTGCGA	1320
GTTGACGAGG	TGACGCGCGG	CGGCGGACCA	GCTCAGGCTC	TCCCGCTGCG	GGAACCGCTC	1380
GAGCAGCGCG	AGTTTGGCGG	CGCAGTCCAG	CAGCTCGCGG	CAATCCATCG	GGTCAACGCTC	1440
GAGCTGATCT	AGCACTGTGT	CCGAGGTTTC				1470

(2) INFORMATION FOR SEQ ID NO:131:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1059 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

5  ATTCGCCATCG CTCGCGCACG TATCACCAGG TACTCGGTTT CGATGGTTT CCGCGGCGCT 60
   TCGGTTGAGC TGGGCCACGG GTGCTTCATG GCGCTCTCTG TCGGAGTTGG AATTGTGTAC 120
   AACGAAATCG GCGGTTGCGT GAGCAATCGT CCGCGATGCA AGACACGCTT TCGCTGCGCG 180
   GCGCTCAGGT GGAGTTAGG CCAGCTAAC AACGTAGACC GCGCACTGAC CAAACCCCAA 240
   ACCGACAAAC CTGCGACGCA TCGGGTCTC GCGCTCAAA TTCCGGGTAG ATATCGTATA 300
10  CCGATATCGG ATGCGCTTAC UTTATCGAGG CAGTGAACCG CCGCTAGACC CAGCGCATAT 360
   TCCAGATGAG CTGCGACGAC GCGTGGGGCT CTGGGATGCG GTGGTGTGCG GCGTTGGGTC 420
   CATGATCGGT GCGGGAATCT TTGCTCTGTC CGATTTGCGG ACGAGCTCGT GCGGAATTCG 480
   GCACGAGATT CCAATCCCCA GAGGCTCGTA CAGGCGCTCA ATGGCACTTG ATCGTTGGAT 540
   CGATGATGAA CGCTCTGCTC ATGCTGCGCG CCAATCTCAA CGTCTGCTGA TTCCATGCAT 600
15  TAGCCTTTGT TCTGCAATGC ACGCGTAGGG CCTACAGTCT GCGTGTGATG CTGGGCGGAT 660
   GTCAACAGCT TTTTTCATGC TAAGCAGATC CTCAGTTTTC AGTTCTGTGA GAGGCGCATGT 720
   TCACTGTGTT TCGACTACAT CGTCTCGCGA CATTTGCGCT CCGTCAACTG CGCTCGGACA 780
   ATGCGCGTAC CCGCTGTGAG CTGCTGCGGA ATTGCGGACG AGGATCCACC GAGATGCGGC 840
   GACGACTACG ACGAGGCGCT GATGCTCAGC ACCGTGTTCG ACTATCAAAA CAGGAACGCA 900
20  AAGAAAGAGG TCATCATCTT CTGCTCCGAC GTGAACAAAG AGAGGGGGGC CATCCAACTC 960
   GTAACCGAGG TAGACAAA GCGACATCAG ACTGCTCTAC GATGCGGAGC CACGTTTTC 1020
   TACAGGAAC ATCCTAAGTT TTGATTCGGG AACATCCTA 1059

```

(2) INFORMATION FOR SEQ ID NO:132:

```

25  (1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 153 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
30  (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

35  GCACGAGGCA TTGCGCGGCA TCTGCATAAA CGGTGACGTA TCACACAAA ACAGCGGAGA 60
   GAACACATCT CGATCAGAAC GTCTCGGCTG GCTGCTAGCC GCAGAGGCTC CCGTCCGCTC 120
   GGTGTATTTT GAGGACTCGC AGGACTCGTG CCG 153

```

(2) INFORMATION FOR SEQ ID NO:133:

```

45  (1) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 387 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

50  CCGCGCGGTC GATCAGCGAG CCAAGCAAAA ACTCGGTGCA GCGGAGTGG ATGATGCTCA 60
   CCGGCGGAGG CATCTGGGGA AGGATCAGCT CGATGTGCTT GTGCTGGATC GACACACCTT 120
   GCGCGCGGTA GAGCTCTCTG ACCTCGCGAA CCAAGGTGAT CTGACACTCG CCGGGGCGCT 180
55  GCGCGCGGAG CAGCTCTCTG GGTCTGCGCG AGCTTCCCAT CAGTGTGCTG CCGACTTGGA 240
   CCGTGTGCGC ATCGGAGAGC ACCCGTTCGG AACCGTCTC GTGCTTGAAC ACCCGAGGAC 300
   CTGCGCGCTT GGAGATCTTG TCGTAGACCA CTTCCTCAAG GCGCTCGTCA GGAACGATGG 360
   TATCTCTGTA GAACCGCTCG CCGTCTCT 387

```

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

5	GTTCAGCAGC	GCTATCCGAT	TGTGCGGTTC	GCTTCGGTGG	GTGCTGAACA	CGGCATCGAC	60
15	ATCGTGCTCG	ACAAACGAATC	CCCACTGCTG	GCACCGGTCC	AGTTCTCTGC	CGAGAAAGTG	120
	CTCGGACGCA	AAGACGGTCC	GGCAGTGGTC	CTGTGTGTGC	GACTGACACC	GGTACCGCGC	180
	CCCGAACGGC	AGTATTACTG	GTTCGGCGAG	CCACACGACA	CCACAGAGTT	TATGGGGGAG	240
	CAAGCGGAGC	ATAACGGGCG	ACCGAGGGTG	CGCGAGCGTG	CGCGCCCGCG	TATCGAACAC	300
	GGCATCGAGC	TGATCTCGGC	CGAGCGGCGA	GGGATCCAA	ATCGATCCCT	GTTCGGACGG	360
20	CTCTCCGCT	CGACGCTTA	AGCGCGCCC				389

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

35	CCCGCGGTGC	GAATGATCCC	CGTCTGCTGC	CGCGCCCAT	TGATGCTGTT	GATGAGGTGT	60
	TTGGAGAAAGC	CGGGTTGGCG	TACCGGTGAG	CCGGAATATC	TGTTGGAAGC	GTCAACGGAT	120
	GTTCACATGA	ATTTCCTTGN	CCGCTTGGCG	GTCTTGTGTC	NGGAAACAC	GTGTTTNTTA	180
	AGCCTTGATG	GTCTGAAAG	NGCGTTGAGC	GGCTGTGTC	CGAAGATATA	TGAGCAGCTG	240
	ACGTTGGGCG	CGATCGCGGT	TATCCCAAGG	AATTCGAGG	TGGTCCCGG	AGATCCCGAA	300
	GGCTTCGAGG	GTCTGTGTCG	CGCTGTGCGG	TCCGTCAAC	CACCTGGCGA	GGGATGTGNN	360
40	AGCCCCGGCG	ACGCTGACAC	CGAGATCCCG	CGCGCCCGCG	CGAGCAGGGT	CGGNNCTGNN	420
	NCCTGNTTCC	TGNGGCGAA	TTNNATCCN	NCNACRANT	TGNNKCGAC	TGNNKCGCGN	480

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

55	GCACGAGGCT	ACCGGCGCGT	CGCCCCCAT	GCCTGGATG	CACGCTTAC	CACCGCTNCA	60
	TNCAGCGGGT	CAGCGGCGCG	GTCCGGGCTT	AACGCTATAG	CAGCTGCAAA	CAACCCAGCG	120
	CCGCGAATTA	CTTTGATGTT	GAACCGATGA	CCATGCGCTN	CGGTGTCAT	CTGCTCTCTT	180
	NCGCGCGCCG	TATTTGGGCC	AGAAATTTGG	TTNNANCGCN	AACCTGAGAC	GTATCGAGTT	240

5
 CCGTTTGCAG CACCGGCTCA ATTGTGAGCA TCCTATGGGG AACATGAGCC GCGCCGCGCC 300
 GGGCGGCTTC CAAATGGTGA GTTCACACCG GTGTACACAG CCGCGCGCAT GTCCCGGGTA 360
 GGGACGCGCG GCGTGGGATC GGTGGGGTGA GCGCTCGGCT TCCTCAAGCG AGGGGAGGCC 420
 CGGGACTCTT ACCGCGCGAA GCGGGCGGGT GTCACTGATC TAGGCTGACG GCCATGTBTT 480
 GNTAGCCGCA CAGCGATGAC NACAATAAAN CCGAGGAGAG ACANNGAGAG GNCGGANAG 540
 CTANCCCGN NTTGNACNAA NNNNACNCAC TTNACCGNN CTATTGN 587

(2) INFORMATION FOR SEQ ID NO:137:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1200 base pairs
 (B) TYPE: nuclear acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

20 CAGGCGATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GCGTGTGACG 60
 ACCTTCTGGG GATTGGGATA CCCAACCAAG GGGGTATCCT TTACTGCTCA CTAGAGTACT 120
 TCGAATAAAGC CCTGGAGGAG CTGGACACAG CGTTTCCGGG TGAATGGCTGG TAAAGTTGGG 180
 CGCGCGAGAA ATACGCGCGG AAAAACCUGA ACCACGTGAA TTTTTCACG GAACTTGGCA 240
 ACCGTGATCG TCAGCTCATC AGCTTGATCC ACGACACAGC CAACCGCGTC CAGACGACCC 300
 25 GCGACATCAT GAGGCGCGCC AAGAAAGGTC TCGAGTTCGT CGCGCCGCTG GCTGTGGGAC 360
 TGACCTAGCT CCGGCTGATC GGCGACGCCC TATCGCGCGC CTTCACGGCG CCGTTTTCGG 420
 CGGGCGCGAT GCGCTGATG GCGCGCGCGC TTGCTACTT GGTGCTGAAA ACCTGTGATCA 480
 ACAGGACTCA ACTCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCCGG GCGCGCATTC 540
 30 GCGACATCAT TTGCGATGTC GCGGACATCA TCAAGGCGAC CCTCGGAGAA GTGTGGAGAT 600
 TCATCATCAA CCGCTCAAC GCGCTCAAG AGCTTTGGGA CAGGCTCAGC GGTGCTGAGA 660
 CCGGACTGTT CTCTCGAGG TGGTCGAACC TGGAGTCTTT CTITGCGGCG GTCCCGGCT 720
 TGACCGCGCC GACCGAGGCG TTGTGCGAAG TGACTGGCTT GTTCGCTGCG GCGGCTGTGT 780
 CGCGATCTCT GGGCTTGGCT CACGCGGATA GCTTGGCGAG CTCAGCCAGC TTGCGCGGCC 840
 TGGCGCGCAT TGGCGCGCGG TCCGTTTTCG GGGCTTTCG GAGGCTTGCT CAGGCTCCTG 900
 35 CCGCTCAAC TCGGCGAGCG CTACCGCGCC GAGCTGATG CCGGCTGCGC GCGCTTGGCG 960
 AGCAGGTCCG CCGGCGATCG CAGCTGCTCT CGCGCGAGCG TTCCCAAGGT ATGGCGGAGC 1020
 CCGTAGGCAT GGGCGGATG CACCCCTCTT CCGGCGCGCT GAGAGGGAGC ACGACGAGA 1080
 AGTACTTCGA AGGCGCGCGC GCGGCGACTG AAGACGCGA GCGCGCGCCA GTGGAAGCTG 1140
 40 ACGCGCGCGG TGGCGAAGG GTCTGCTAC GAAACGCTCT CTAAGGCAT GCGGAGCCAA 1200

(2) INFORMATION FOR SEQ ID NO:138:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 55 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Gln Glu Leu Ala Ala
 35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
55 65 70 75
5 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110
10 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115 120 125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130 135 140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160
15 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180 185 190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195 200 205
20 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210 215 220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225 230 235 240
25 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245 250 255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260 265 270
30 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275 280 285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Glu
290 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305 310 315 320
35 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350
40 Lys Gly Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380
Lys Val Leu Val Arg Asn Val Val
385 390

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACGTTTACCC ATGCCGTCGG TGCAGAGCAA CCCCAGACAA CACAAATAG TTTATTTCC

60

1TTATAAAGCA GACATTTCGG TGOTTATGTA GAAGATGTGG ACCGATCAGA TGAACCGATC 120
 CGGCTCAGGT GGTATCCGAT GTCTTTTGTG ACCATCCAGC CGGTGCTCTT GGCACCCCGG 180
 ACGGCGGACT TCGGACGAT CGGTACCGCT GTGAGTGCTC GGRACACAGC CGTCTGTGCT 240
 CCGACACGGG GGGGTGTACC CCTCTGTCG AATGACGTGT CGGTCTTAC GCGCGCCCGG 300
 5 TTCACCGCGC ACACCAAGCA CTACCGAGTG GTGAGTAAGC CGGCCCGGCT GGTCCATGAC 360
 AACTCTGTGG CCTTCCCGGC GGCACCGCC GATGCGTATG CGACCAACCGA GGCCTCTCAT 420
 GTGTCGCGCA CGGTTTAAG 439

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTCTGG GCAATGATG TCGGCTTTT ACCTCCGAA GTGAATTCRA GCGGAATGTA 60
 TTCGGTTCGG GGGCCGGAGT CGATGCTAGC CCGCCCGGCC GCTTGGGACG GTGTGGCCGC 120
 GGAATGTACT TCGGCGCGCG TCTCTGATGG ATCGGTGCTG TCGACGCTGA TGGTTGAGCC 180
 25 GTGATATGGG CGCGCGCGCG CCGCGATGCG GCGCGCGCA ACGCGGTATG TGGGGTGGCT 240
 GCGCGCGCAG CGCGCGCTGG CGAGAGGAGC GCGCACACAG CGGAGGGCAG CGGCGGAGCG 300
 GTTTGCGACG GCGTTCCGGA TGACGCTGCC ACCATCTCTC GTGCGCGCCA ACCGCGAGCG 360
 GTTGAATGTC GTGGTCCGGG CGAACATCTT GGGGCAAAAC AGTGCGGCGCA TCGCGGCTAC 420
 CCAGCGCGAG TATGCGCGAA TGTGGGCGCA AGACGCTGCC GTGATGTACA GCTATGAGGG 480
 GGCATCTGCG CGCGCGCTGG CGTTGCGGCC GTTCACTCCA CGCGTGCAGG GCACCGGCGC 540
 30 GCGCGCGCCC GCGCGCGCAG CCGCGCGAC CGAGCGCGCC GGTGCGCGCG CGGTGCGGGA 600
 TGCACGCGCG ACACGTGCGC AGCTGCGCCC GCGGATCTGT AGCGACATTC TGTCCGCTTT 660
 GCGCGCGCAC GCTGATCCCG TGACATCGGG ACTGTTGGGG ATCGGCTCGA CCTCTCAACC 720
 GCGAGTCTGA TCGGCTGAGC CGATAGTATG CCGCACCGCG ATAGGGGATAT TGGACGTGAT 780
 CGCGCTCTAC ATTGATCTCA TCGCGACCGG CAGCATCTCG CTGCGGATCA CGAAGACGGC 840
 35 CAGACCTTGG CACATCGGCC TATACGGGAA CGCGCGCGCG CTGGGACCGA CGCAGGCGCA 900
 TCCACTGACT TCGGCGACCG ACGAGCGGGA GCGCGACTGG GCGCGCTTGG GGGCGCGCGC 960
 GCGCGGTGCG CGCGCGGTGG GCGACCGAGC ATTAGTGGGA CGGTGCTGGG TGCGCGACAG 1020
 CTGGACACCG CGCGCGCGCG AGATCCAGGT CGCGGTTCAG GCGACACCCA CTTTCAGCTC 1080
 CAGCGCGCGC GCGACCGGGA CGGCGCTAAA CGGATGCGG CGAGGCTTGC TCAGCGGAT 1140
 40 GCGTTTGGCG AGCCTGCGCG CAGCGCGCAC GCGCGGCGGT GCGCGGCGCC GTAGCGGACG 1200
 CAGCATGTAC GCGCAAGAGG ACGCGCGGCA AGCGCGGTA GTTGTGATTA GAGACGACCG 1260
 GCGCGCGGGA AACCGCGCGC GGTAAAAATC CGCGACCGGT GTGTGCGCGC GCGGAAATG 1320
 CCGGTGTAGC GTGCGCTATC GACGCGCGGT TCACACCGCT TGTAGTAGCG TACGCGTATG 1380
 45 GACGACGGTG TCTGTATCT CGCGCGCTAT CAGAGCGATG TTGCTCGGCA CCTCAGCGAA 1440
 G 1441

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Ser Phe Val Thr Ile Gln Pro Val Val Leu Ala Ala Ala Thr Gly
 1 5 10 15
 Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
 20 25 30
 5 Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asn Asp Val Ser
 35 40 45
 Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
 50 55 60
 10 Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
 65 70 75 80
 Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val
 85 90 95
 Ala Thr Gly

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(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 423 amino acids
 20 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1 5 10 15
 30 Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
 20 25 30
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 35 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
 85 90 95
 40 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 45 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 50 Ala Gly Pro Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 55 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile

245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Gln
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

25 (2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Ser Gly Ulu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

50 (2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:144:

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Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1           5           10           15
Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
 20           25           30
10 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
 35           40           45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
 50           55           60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
 65           70           75           80
15 Gln Xaa Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
 85           90           95
Ala Ala Gly

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